OIPE

RAW SEQUENCE LISTING DATE: 03/01/2002
PATENT APPLICATION: US/10/077,040 TIME: 12:43:17

Input Set : N:\Crf3\RULE60\10077040.raw
Output Set: N:\CRF3\03012002\J077040.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Lal, Preeti
Corley, Neil C.
Patterson, Chandra
(ii) TITLE OF INVENTION: HUMAN NEUROSECRETORY PROTEINS
(iii) NUMBER OF SEQUENCES: 6
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
(vi) CURRENT APPLICATION DATA:
C--> **(A) APPLICATION NUMBER: US/10/077,040**
C--> **(B) FILING DATE: 14-Feb-2002**
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 09/062,601
(B) FILING DATE:
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Cerrone, Michael C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0510 US
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 468 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(vii) IMMEDIATE SOURCE:
(A) LIBRARY: ISLTNOT01
(B) CLONE: 2379427

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Gly Phe Leu Gly Thr Gly Thr Trp Ile Leu Val Leu Val Leu Pro
 1               5                  10                  15
Ile Gln Ala Phe Pro Lys Pro Gly Gly Ser Gln Asp Lys Ser Leu His
            20                  25                  30
Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile Ala Glu
        35                  40                  45
Ala Glu Glu Asp Lys Ile Lys Lys Thr Tyr Pro Pro Glu Asn Lys Pro
    50                  55                  60
Gly Gln Ser Asn Tyr Ser Phe Val Asp Asn Leu Asn Leu Leu Lys Ala
65                  70                  75                  80
Ile Thr Glu Lys Glu Lys Ile Glu Lys Glu Arg Gln Ser Ile Arg Ser
                85                  90                  95
Ser Pro Leu Asp Asn Lys Leu Asn Val Glu Asp Val Asp Ser Thr Lys
            100                 105                 110
Asn Arg Lys Leu Ile Asp Asp Tyr Asp Ser Thr Lys Ser Gly Leu Asp
        115                 120                 125
His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp Gly Thr
    130                 135                 140
Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Ala Arg Ile Tyr
145                 150                 155                 160
Glu Glu Asn Asp Arg Ala Val Phe Asp Lys Ile Val Ser Lys Leu Leu
                165                 170                 175
Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu Asp Glu
            180                 185                 190
Val Ala Glu Val Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn Asn Tyr
        195                 200                 205
Glu Glu Asp Pro Asn Lys Pro Thr Ser Trp Thr Glu Asn Gln Ala Gly
    210                 215                 220
Lys Ile Pro Glu Lys Val Thr Pro Met Ala Ala Ile Gln Asp Gly Leu
225                 230                 235                 240
Ala Lys Gly Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr Leu Thr
                245                 250                 255
Asn Gly Leu Glu Arg Arg Thr Lys Thr Tyr Ser Glu Asp Asn Phe Glu
            260                 265                 270
Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Lys Ser Ile Asp
        275                 280                 285
Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile Met Lys
    290                 295                 300
Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr Ile Ser
305                 310                 315                 320
Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Met Ile Ala
                325                 330                 335
Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Ala Thr Asp Asn Ile Ser
            340                 345                 350
Lys Leu Phe Pro Ala Pro Ser Glu Lys Ser His Glu Glu Thr Asp Ser
        355                 360                 365
Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser Leu Lys
    370                 375                 380
```

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Asp Ser Thr Lys Asp Asp Asn Ser Asn Pro Gly Gly Lys Thr Asp Glu
385 390 395 400
Pro Lys Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg Lys Asn Ile
405 410 415
Glu Trp Leu Lys Lys His Asp Lys Lys Gly Asn Lys Glu Asp Tyr Asp
420 425 430
Leu Ser Lys Met Arg Asp Phe Ile Asn Lys Gln Ala Asp Ala Tyr Val
435 440 445
Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Glu Ala Ile Lys Arg Ile
450 455 460
Tyr Ser Ser Leu
465

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1844 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: ISLTNOT01
(B) CLONE: 2379427

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CAGCGCTCCC CTCTACCTGG AGACTTGACT CCCGCGCGCC CCAACCCTGC TTATCCCTTG 60
ACCGTCGAGT GTCAGAGATC CTGCAGCCGC CCAGTCCCGG CCCCTCTCCC GCCCCACACC 120
CACCCTCCTG GCTCTTCCTG TTTTTACTCC TCCTTTTCAT TCATAACAAA AGCTACAGCT 180
CCAGGAGCCC AGCGCCGGGC TGTGACCCAA GCCGAGCGTG GAAGAATGGG GTTCCTCGGG 240
ACCGGCACTT GGATTCTGGT GTTAGTGCTC CCGATTCAAG CTTTCCCCAA ACCTGGAGGA 300
AGCCAAGACA AATCTCTACA TAATAGAGAA TTAAGTGCAG AAAGACCTTT GAATGAACAG 360
ATTGCTGAAG CAGAAGAAGA CAAGATTAAA AAAACATATC CTCCAGAAAA CAAGCCAGGT 420
CAGAGCAACT ATTCTTTTGT TGATAACTTG AACCTGCTAA AGGCAATAAC AGAAAAGGAA 480
AAAATTGAGA AAGAAAGACA ATCTATAAGA AGCTCCCCAC TTGATAATAA GTTGAATGTG 540
GAAGATGTTG ATTCAACCAA GAATCGAAAA CTGATCGATG ATTATGACTC TACTAAGAGT 600
GGATTGGATC ATAAATTTCA AGATGATCCA GATGGTCTTC ATCAACTAGA CGGGACTCCT 660
TTAACCGCTG AAGACATTGT CCATAAAATC GCTGCCAGGA TTTATGAAGA AAATGACAGA 720
GCCGTGTTTG ACAAGATTGT TTCTAAACTA CTTAATCTCG GCCTTATCAC AGAAAGCCAA 780
GCACATACAC TGGAAGATGA AGTAGCAGAG GTTTTACAAA AATTAATCTC AAAGGAAGCC 840
AACAATTATG AGGAGGATCC CAATAAGCCC ACAAGCTGGA CTGAGAATCA GGCTGGAAAA 900
ATACCAGAGA AAGTGACTCC AATGGCAGCA ATTCAAGATG GTCTTGCTAA GGGAGAAAAC 960
GATGAAACAG TATCTAACAC ATTAACCTTG ACAAATGGCT TGGAAAGGAG AACTAAAACC 1020
TACAGTGAAG ACAACTTTGA GGAACTCCAA TATTTCCCAA ATTTCTATGC GCTACTGAAA 1080
AGTATTGATT CAGAAAAAGA AGCAAAAGAG AAAGAAACAC TGATTACTAT CATGAAAACA 1140
CTGATTGACT TTGTGAAGAT GATGGTGAAA TATGGAACAA TATCTCCAGA AGAAGGTGTT 1200
TCCTACCTTG AAAACTTGGA TGAAATGATT GCTCTTCAGA CCAAAAACAA GCTAGAAAAA 1260
AATGCTACTG ACAATATAAG CAAGCTTTTC CCAGCACCAT CAGAGAAGAG TCATGAAGAA 1320
ACAGACAGTA CCAAGGAAGA AGCAGCTAAG ATGGAAAAGG AATATGGAAG CTTGAAGGAT 1380
TCCACAAAAG ATGATAACTC CAACCCAGGA GGAAAGACAG ATGAACCCAA AGGAAAAACA 1440
GAAGCCTATT TGGAAGCCAT CAGAAAAAAT ATTGAATGGT TGAAGAAACA TGACAAAAAG 1500
GGAAATAAAG AAGATTATGA CCTTTCAAAG ATGAGAGACT TCATCAATAA ACAAGCTGAT 1560
GCTTATGTGG AGAAAGGCAT CCTTGACAAG GAAGAAGCCG AGGCCATCAA GCGCATTTAT 1620

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PATENT APPLICATION: US/10/077,040 TIME: 12:43:17

Input Set : N:\Crf3\RULE60\10077040.raw
Output Set: N:\CRF3\03012002\J077040.raw

AGCAGCCTGT AAAAATGGCA AAAGATCCAG GAGTCTTTCA ACTGTTTCAG AAAACATAAT 1680
ATAGCTTAAA ACACTTCTAA TTCTGTGATT AAAATTTTTT GACCCAAGGG TTATTAGAAA 1740
GTGCTGAATT TACAGTAGTT AACCTTTTAC AAGTGGTTAA AACATAGCTT TCTTCCCGTA 1800
AAAACTATCT GAAAGTAAAG TTGTATGTAA GCTGAAAAAA AAAA 1844

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRSTTUT14
(B) CLONE: 2744187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Ala Ala Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala
1 5 10 15
Ala Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser
20 25 30
Phe Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro
35 40 45
Pro Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu
50 55 60
Asn Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro
65 70 75 80
Val Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser
85 90 95
Ile Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr
100 105 110
Arg Met Lys Glu Trp Ser Arg Arg Glu Ala Glu Arg Leu Val Lys Tyr
115 120 125
Arg Glu Ala Asn Gly Leu Pro Ile Met Glu Ser Asn Cys Phe Asp Pro
130 135 140
Ser Lys Ile Gln Leu Pro Glu Asp Glu
145 150

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1463 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRSTTUT14
(B) CLONE: 2744187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CAGCCGCTGG CTCCGTTTCA CTTCCCAGCC ACCCCCGCTG CTGCTACCAT GATCTGCCAG 60
CCTGGGTGAT GCTTCCTGCA GGGACTCTTC TCGGCCCGGG CTGTCAAGGA AGGGCTCCCA 120
GACATCACCT CTGCCCGCCG CCACCTCCTC CAACTCTCCC AGCTCAGCCG GAGCCGGAGC 180
GCGCAACAAC CAAGTCCGAG ACTGGAGGCA GATCGGGGGG AGGGGAGAAG CGCCAAGCGC 240
GCTGCCCTCC CAGGGAAACT CACTGCCGCC TACTCCCAGC CGGCCACAGT CACCAGCTCA 300

RAW SEQUENCE LISTING DATE: 03/01/2002
PATENT APPLICATION: US/10/077,040 TIME: 12:43:17

Input Set : N:\Crf3\RULE60\10077040.raw
Output Set: N:\CRF3\03012002\J077040.raw

223 AAATGGCGAC GACGAGAAGG GAGTCGGCGC TCCGACCACC ATCCACCTAC TAAGGAAGCG 360
224 CGCTCTGGCC GGCCCCGGCG ATTGGTCACC GCCCGCTAGG GGACAGCCCT GGCCTCCTCT 420
225 GATTGGCAAG CGCTGGCCAC CTCCCCACAC CCCTTGCGAA CGCTCCCCTA GTGGAGAAAA 480
226 GGAGTAGCTA TTAGCCAATT CGGGCAGGGC CCGCTTTTTA GAAGCTTGAT TTCCTTTGAA 540
227 GATGAAAGAC TAGCGGAAGC TCTGCCTCTT TCCCCAGTGG GCGAGGGAAC TCGGGGCGAT 600
228 TGGCTGGGAA CTGTATCCAC CAAATGTCAC CGATTCTTCC TATGCAGGAA ATGAGCAGAC 660
229 CCATCAATAA GAAATTTCTC AGCCTGGCCG AAAATGGTTG GCCCCACGAA GCCACGACAA 720
230 CTGGAGGCAA AGAGGGTTGC TCAACGCCCC GCCTCATTGG AAAACCAAAT CAGATCTGGG 780
231 ACCTATATAG CGTGGCGGAG GCGGGGCGAT GATTGTCGCG CTCGCACCCA CTGCAGCTGC 840
232 GCACAGTCGC ATTTCTTTCC CCGCCCCTGA GACCCTGCAG CACCATCTGT CATGGCGGCT 900
233 GGGCTGTTTG GTTTGAGCGC TCGCCGTCTT TTGGCGGCAG CGGCGACGCG AGGGCTCCCG 960
234 GCCGCCCGCG TCCGCTGGGA ATCTAGCTTC TCCAGGACTG TGGTCGCCCC GTCCGCTGTG 1020
235 GCGGGAAAGC GGCCCCCAGA ACCGACCACA CCGTGGCAAG AGGACCCAGA ACCCGAGGAC 1080
236 GAAAACTTGT ATGAGAAGAA CCCAGACTCC CATGGTTATG ACAAGGACCC CGTTTTGGAC 1140
237 GTCTGGAACA TGCGACTTGT CTTCTTCTTT GGCGTCTCCA TCATCCTGGT CCTTGGCAGC 1200
238 ACCTTTGTGG CCTATCTGCC TGACTACAGG ATGAAAGAGT GGTCCCGCCG CGAAGCTGAG 1260
239 AGGCTTGTGA AATACCGAGA GGCCAATGGC CTTCCCATCA TGGAATCCAA CTGCTTCGAC 1320
240 CCCAGCAAGA TCCAGCTGCC AGAGGATGAG TGACCAGTTG CTAAGTGGGG CTCAAGAAGC 1380
241 ACCGCCTTCC CCACCCCCTG CCTGCCATTC TGACCTCTTC TCAGAGCACC TAATTAAAGG 1440
242 GGCTGAAAGT CTGAAAAAAA AAA 1463
244 (2) INFORMATION FOR SEQ ID NO: 5:
246 (i) SEQUENCE CHARACTERISTICS:
247 (A) LENGTH: 471 amino acids
248 (B) TYPE: amino acid
249 (C) STRANDEDNESS: single
250 (D) TOPOLOGY: linear
252 (vii) IMMEDIATE SOURCE:
253 (A) LIBRARY: GenBank
254 (B) CLONE: 413764
256 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```
Met Gly Phe Leu Trp Thr Gly Ser Trp Ile Leu Val Leu Val Leu Asn
 1               5                  10                  15
Ser Gly Pro Ile Gln Ala Phe Pro Lys Pro Glu Gly Ser Gln Asp Lys
            20                  25                  30
Ser Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln
        35                  40                  45
Ile Ala Glu Ala Glu Ala Asp Lys Ile Lys Lys Ala Phe Pro Ser Glu
    50                  55                  60
Ser Lys Pro Ser Glu Ser Asn Tyr Ser Ser Val Asp Asn Leu Asn Leu
65                  70                  75                  80
Leu Arg Ala Ile Thr Glu Lys Glu Thr Val Glu Lys Glu Arg Gln Ser
                85                  90                  95
Ile Arg Ser Pro Pro Phe Asp Asn Gln Leu Asn Val Glu Asp Ala Asp
            100                 105                 110
Ser Thr Lys Asn Arg Lys Leu Ile Asp Glu Tyr Asp Ser Thr Lys Ser
        115                 120                 125
Gly Leu Asp His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu
    130                 135                 140
Asp Gly Thr Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Thr
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VERIFICATION SUMMARY DATE: 03/01/2002
PATENT APPLICATION: US/10/077,040 TIME: 12:43:18

Input Set : N:\Crf3\RULE60\10077040.raw
Output Set: N:\CRF3\03012002\J077040.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]